

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2001, 09:44:54 ; Search time 2029.33 Seconds
(without alignments)
12851.804 Million cell updates/sec

Title: US-09-784-340-1

Perfect score: 2759

Sequence: 1 caaccatgcgcacatgctgt.....ctgcacgccttaagtagcg 2759

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 10228115 segs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

BASE COUNT 618 a 406 c 467 g 608 t
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Query Match 32.08; Score 882.8; DB 192; Length 2099;
Best Local Similarity 73.48; Pred. No. 1e-177;
Matches 1173; Conservative 0; Mismatches 412; Indels 13; Gaps 3;

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11 CAATATGCTCTCGAAAAATGTGTGGGCAATTTTCTGCTGAGCTTGTGGCGG 70
94 ctgtgattcttgcgaaagctcctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 153
71 CTGTGATTCGTGACGAAAGTCTCGTGTGGCTGTGATATGACGACGCTGATCT 130
154 caaggtcattctgaagagctcatgtgagagcattgaagtaagtaagtaagta 213
131 AAGACTATTCCTTGAGAGAGCTTGAGACAGAGGAGGACAGAGTAAAGTCC 190
214 aaagccttcgttaattgactacagagagccttcgtcattgaattgaagtgat 273
191 CA---GTATCATATGATATGATGAGTAAAGTAACTTCCACTTGTGAAATTCCTTT 247
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QY 985 agaaagagcattatcatctgttcagcccttgccagatccacagaaagtgatagag 1044
DB 968 AGAAGAGCCAACTCATTCCTCTGTCCTTGCCCAATTCGCCAGAGGTTTGTGGAG 1027
QY 1045 gtacaaagaaanaaaacacatccatctagagagcacaactcgcgtgatgtatgatacc 1104
DB 1028 ATATCTGAGGAGAGAGGACGACCAATATGATCAATACCTCGGCTTTTAAATGATTC 1087
QY 1105 ccgaatagatctctgtgtcatcccaacaaagcattatcaactaagtggtgaatga 1164
DB 1088 CCAGAAATGATCTTCTTGAGATCTCTAAACCAAGCTTTCATCAACATGCTGGAACAAA 1147
QY 1165 tggatctatgaagcattatccatgaggtcccatgagtgagtgaggttccatattgtga 1224
DB 1148 CGGATTTATGAAGCCATTACCATGAGGCTTATGTTGCTGCTTCCATGTTAGGGGA 1207
QY 1225 tcaagttgataatagctatcatcacaatgaagagcagagcgtgtagaataaactca 1284
DB 1208 TCAGCCTCAGCAACATCGCTCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1267
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RESULT 2
AK004971
LOCUS 2573 bp mRNA HTC 08-FEB-2001
DEFINITION Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300012D20, full insert sequence.
ACCESSION AK004971
VERSION AK004971.1 GI:12836559
KEYWORDS CAP trapper.
SOURCE Mus musculus (strain: C57BL/6J) adult male liver cDNA to mRNA, clone:1300012D20.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods Enzymol. 303, 19-44 (1999)
2 (sites)
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
3 (sites)
JOURNAL MEDLINE
20499374
REFERENCE
AUTHORS Kono, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M.,

Db	1162	GAACCAATGGCATTCATATGAGCGGATCTACCATGCGATTCCTATTGTTGGTATTCCTTGT	1221
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Db	1282	ACTTGTGATACAAATGTCAACCTACAGACCTTCTCACGCGCTTGAAAGCTGTCAATTATGACC	1341
Qy	1338	cccttataaagaagatgctatgagattatacaagattcacatgatacactgtgaagc	1397
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Qy	1458	tgcgatacagctgcgccatgaacctaacccgtgttcagcagcactactatgatgtgattgggt	1517
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RESULT	3		
AK002736			
LOCUS	AK002736	1896 bp	mRNA
DEFINITION	Mus musculus adult male kidney cDNA, RIKEN full-length enriched		HTC 08-FEB-2001
ACCESSION	AK002736	library, clone:0610033E06, full insert sequence.	
VERSION	AK002736.1	GI:12832933	
KEYWORDS	CAP trapper.		
SOURCE	Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone:lib.RIKEN full-length enriched mouse cDNA library		
	clone:0610033E06.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (sites)		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Methods Enzymol. 303, 19-44 (1999)		
REFERENCE	2 (sites)		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
REFERENCE	20499374		
AUTHORS	3 (sites)		
	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishik, K., Kitsuana, T., Tashiro, H., Itoh, M., Kikuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Okazaki, Y., Muramatsu, M., Inoue, Y., and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
REFERENCE	20530913		
AUTHORS	4 (sites)		
	The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		

REFERENCE
AUTHORS

5 (bases 1 to 1896)
Adechi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Carinacci,P., Fukuda,S., Fukunishi,Y., Furuno,M.,
Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F.,
Imotani,K., Ishi,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J.,
Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T.,
Miyazaki,A., Nishi,K., Nomura,K., Oka,S., Okazaki,R., Ohno,M., Okazaki,Y.,
Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H.,
Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A.,
Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (10-Jul-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama
kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGGAGGAGCGGCCGCACCTCAGATTTTATTTTATTTTATTA 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to Rot = 5.0. Second strand cDNAs
was prepared with the primer adapter of sequence [5'
GAGGAGGAGGAGCATCAAGACTCAATTATTTATTTATTAACCCCCCCC 3']. cDNA was
cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
XhoI. Host: SOBR.

FEATURES
source

Location/Qualifiers

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/db_xref="gi:12832934"
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IAELHLPEIYSIRLEFTAGYRIEKSSRGFLPRSVPIITSLGSQMDFIFRRNMICM
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CDS

BASE COUNT
ORIGIN

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Query Match 22.6%; Score 623; DB 192; Length 1896;
Best Local Similarity 63.3%; Pred. No. 2,je-122;
Matches 1013; Conservative 0; Mismatches 570; Indels 18; Gaps 3;

Dbb 63 tatcttgctcgcgacgtcttcctcgctgctgctgctgctgctggaaagccctggt 122
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TGTTGCTTCGCAATAAGTTCGTCTCGATCTCGAATTCGCAATGCGGAAGTGTGGTGT 120

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Qy	243	cttcctcatctgaaatttgaagtgggtccatactgcacagagcagaacagaagaatgaa	302
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Db	838	CTCACCCGACCTTACCAAAATGTGACTATGTTGGAGAGCTCCACATGCAAACTGCTATAAC	897
Qy	891	cttgcctaaggaagaatggaaaatttgcctcagaagttcaggggaagaatgtatgtgagct	950
Db	898	CTTTGCTCTAAGGATGTGAAGAAATATGTCCAGAGCTCTGTGAACAACATGGTGTAGTGCT	957
Qy	951	ttctctcggggtcaactttcaaatggttacagaagaagaagctaatatcatctgttcag	1010
Db	958	TTTCTCTTGGGTCAATGCTTATGTAACATCAGCAAAATAAATTCMAACGCAATGGATGGG	1017
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ACCESSION	HS_3141_A2_H04_TTC C17 Approved Human Genomic Sperm Library D Homo
VERSION	AO784447
KEYWORDS	sapiens genomic clone Plate=3141 Col=8 Row=0, DNA sequence.
ORGANISM	AO784447.1 GI:5692071
SOURCE	GSS.
REFERENCE	human.
AUTHORS	Homo sapiens
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	1 (bases 1 to 595)
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
	Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and
JOURNAL	scanning the human genome
MEDLINE	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
COMMENT	99380589
	Contact: Mahairas GG, Wallace JC, Hood L
	High Throughput Sequencing Center
	University of Washington
	401 Queen Anne Avenue North, Seattle, WA 98109, USA
	Tel: (206) 616-3618
	Fax: (206) 616-3887
	Email: jwallace@u.washington.edu
	Clones may be purchased from Research Genetics (info@resgen.com).
	BAC end Web Server: http://www.htsc.washington.edu
	Plate: 3141 row: 0 column: 8
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1821 tctactcttgacacagaagacatgatactcaattcttcattctgatactctg 1880
Db TCTCAGCTGTGACTCTTGTGACATGATACATCAATTTCTCTATATCTGATACCTG 145
1881 tttccatgaagctactactctccttaacctaagtataggggtgacccgatactg 1940
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1941 tctctggtttgacacacacatgagatgataaagaatgataaattgataaatt 2000
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2001 tcaagtaac 2060
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2061 atgattcttcttcaatttaataagcccttctacatacccaagcattactgact 2120
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2121 acaatgaattgctaaataagacatagggcattacactcagaatagttgctatctc 2180
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DEFINITION 602463689p1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4593694 5',
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VERSION BG402144.1 GI:13295592
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsab-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LCM1314 row: a column: 23
High quality sequence stop: 557.
Location/Qualifiers

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QY	2165	agttgcctatatcttcacatcactcatcagttcagttcagatagcctaacattcttcgca	2219
Db	656	AAGTTGGTGGTTTCCCTGACCCACCTTAATGTCGGGCGCATTTTGTGCCCA	710
RESULT	6		
LOCUS	BF689099/c		
DEFINITION	BF689099	823 bp	mRNA
ACCESSION	6021851721	NIH_MGC_43	Homo sapiens cDNA clone IMAGE:429880 3',
VERSION	BF689099		mRNA sequence.
KEYWORDS	BF689099.1	GI:11974507	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
JOURNAL	1 (bases 1 to 823)		
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: csapbs@mail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Ling Hong/Rubin laboratory		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/MLN at:		
	http://image.lnl.gov		
	Plate: LCM1157 row: 0 column: 17		
	High quality sequence start: 5		
	High quality sequence stop: 796.		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:429880"		
	/clone_lib="NIH_MGC_43"		
	/tissue_type="normal pigmented retinal epithelium"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: eye; Vector: pORF7; Site: 1: XhoI; Site: 2:		
	EcoRI; cDNA made by oligo-dT priming. directionally		
	cloned into EcoRI/XhoI sites using the following 5'		
	adaptor: GGCACGAG(G). Library constructed by Ling Hong		
	in the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies).		
	Note: this is a NIH_MGC Library. "		
BASE COUNT	221 a 199 c 164 g 239 t		
ORIGIN			
Query Match	17.3%; Score 477; DB 168; Length 823;		
Best Local Similarity	78.0%; Pred. No. 2.4e-91;		
Matches	587; Conservative 0; Mismatches 165; Indels 1; Gaps 1		
QY	876	gtaaacctgcgaagcttgcctaaagaaatgaaatttgcgaagttcgaaggaag	935
Db	804	GCACCGCGCCCAACCCCTGCCTTAAGGAATGGAAGACTTTGTACAGAGTTCTGGAGAA	745
QY	936	atggtatgtgtgtgttctctctggtgtgtacgtttccaatgtttacagaagaagcta	995
Db	744	ATGGTGTGTGGTGTCTTCTCTGGGGTCAATGTGTCAAGTAACTGACAGAAAGGGCCA	685
QY	996	atatactgtctcaagcctctgccagatcccaagaagtgatgtatgagagttacaaagaa	1055
Db	684	ACGTAATTGTCATACACCTCGGCCCGAGATCCACAAAGAGTCTGTGAGAGATTGTATGGA	625
QY	1056	aaaacccatccatattagagaccatattccggtctgtatgtatgtatgataccccaagatgac	1115
Db	624	ATTAACCGAGATACCTTGGTCTCATCTACTCGGCTGTATTAAGAGGAAATCCCGAATGACC	565

FEATURES	source
ORGANISM	Human.
ORGANISM	Human sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ .
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	Email: cgabs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LLAM10287 row: h column: 08 High quality sequence stop: 661.
FEATURES	Location/Qualifiers
1.	671
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/clone="IMAGE:4470199"	
/clone_1b="NIH-MGC_89"	
/russue_type="hypermprroma, cell line"	
/lab_host="DH10B (phage-resistant)"	


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DEFINITION 602185172F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4299880 5',
mRNA sequence.
ACCESSION BF688309
VERSION BF688309.1 GI:11973717
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 746)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apds-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LCM157 row: o column: 17
High quality sequence stop: 707.

FEATURES
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location/Qualifiers
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/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. 1"

BASE COUNT 212 a 158 c 183 g 193 t

Query Match 15.8%; Score 435; DB 168; Length 746;
Best Local Similarity 79.8%; Pired. No. 2e-82;
Matches 574; Conservative 0; Mismatches 140; Indels 5; Gaps 5;

Qy 857 ttgttggaagatgacgtctaaacctgccaagcttgcctaaggaatggaattttc 916
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Db 3 tttgttggaagacctcactgcgaacctgccaacctgcttaaggaattggaaccttt 62

Qy 917 gtccagagttcagaggaagatgcatgtgtttctctggtgacgtttccaagt 976
|||||
Db 63 gTACAGAGCTCTGAGAGAAATGCTGTGTGCTTTCTCTGGGGTCAATGTCAGTAAAC 122

Qy 977 gtaccagaagaaggtatataatctgtctcagcccttgccagatcccaagaagtg 1036
|||||
Db 123 ATGCACAGAAAGAGGCCCAAGCTAATGTCATACGCCCTGGCCAGATCCCAAAAGGTT 182

Qy 1037 ttatgaggtacaaagaaaaaacatccatattagagccaattactcgctttagat 1096
|||||
Db 183 CTGTGGAGATTGTGATGGGAATTAACACAGATACCTTAGCTCAATACCTGGCTGTATTAAG 242

Qy 1097 ttgatacccaagaatgctctctgtgcatcccaaaccaagctttatcaccaatg 1156
|||||
Db 243 TGGATACCCAGATGACCTTTCTAGTCATACCAAGACAGCTTTATTAACATCATGCT 302

Qy 1157 ggaatgaaggagatcatgaagctattaccatgggggtccctatggtggaagtcata 1216
|||||
Db 303 GGAAGCCATGATGATGATGAGGAGCAATCTACCATGGATGCCCTATAGTGAGGATTCATTTG 362

Qy 1217 ttgtgtgatacgtctgtataacatagctccatataagagcaagagcagctgtgaata 1276

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Db 363 tttgccgattcaacctgataaacattgcttcacatgaaagcc agggagcagctgttagaagtg 421
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Qy 1277 aactcaaaactatgacaagcgaagattactgagggctttagaagacagtcataccgat 1336
|||||
Db 422 GACTTCAACACAAATGTGAGTACAGACTTGTGATGATGATGAGAGATTAATTAAGAT 481

Qy 1337 tctctataaagaagaatgcatagataltatcaagaatccatgatcaactgtaag 1396
|||||
Db 482 CTTTCATATAAAGAGAAATGTATGAATTAATCAAGAAATTAATCAATGATCAACAGTGAAG 541

Qy 1397 cccctagtcagagcgtcttgatgcaggttttcattgagcccaagaaggccaagag 1456
|||||
Db 542 CCGCTGATGAGCAGCTCTTGTGATGCAATTTGTGATGCGCCCAAGAGACTTAACAC 601

Qy 1457 ctgcatcagctgcccacatgacctcactggttcagcagcactatagatgattgg 1516
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Db 602 CTTCGGGTGACGCCACGA-CTCACCTGGTTCAGTACCACTCT-TCGATGTGATTGGG 659

Qy 1517 ttctgtgacctgtgtggcaactgtcatatcttctgtcacaagaatgttttatttc 1575
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Db 660 TT-CTGCTGCTGTGTGGGC-ACGTGATATTATTCGCACAAAGTGTGCTGCTGTC 716

RESULT 10
A0441905 446 bp DNA GSS 31-MAR-1999
LOCUS A0441905
DEFINITION HS.5058.B2.B12.SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=634 Col=24 Row=D, DNA sequence.
ACCESSION A0441905
VERSION A0441905.1 GI:4553244
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 446)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@edong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (Info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 634 row: D column: 24
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 446.

FEATURES
Source
location/Qualifiers
1..446
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/db_xref="taxon:9606"
/clone="Plate=634 Col=24 Row=D"
/clone_1lb="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

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DEFINITION	BE0132199	MARC	1P1G	Sus scrofa	cdna 5', mRNA sequence.
ACCESSION	BE0132199				
VERSION	BE0132199.1				
KEYWORDS	EST.				
SOURCE	EST.				
ORGANISM	Sus scrofa				
REFERENCE	Eukaryota; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.				
AUTHORS	1 (bases 1 to 554) Fahrenkrug, S.C., Fickling, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keeler, J.W.				
TITLE	Design and use of two pooled tissue normalized cdna libraries for EST discovery in swine				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt. trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options. PCR primers FORWARD: AGGAACACGCTATGACCAT BACKWARD: GTTTCACGCTACGACGAG Plate: 50 row: G column: 16 Seq primer: ATTGAGCGACACTATGAC. Location/Qualifiers 1..554 /organism="Sus scrofa" /db_xref="taxon:9823" /clone_1lb="MARC 1P1G" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."				
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Query Match	14.5%	Score 399.4;	DB 162;	Length 554;	
Best Local Similarity	83.3%;	Pred. No. 7.6e-75;			
Matches	454;	Conservative 0;	Mismatches 91;	Indels 0;	Gaps 0;
QY	1048	caaaaggaanaaacatccacatattagagagccaaatctcgtctatgtatgtatgccca	1107		
Db	10	CACAGCGAAGAAACCAAGAAACATTTAGGAGCCATCTCGGCTGTATGATGATGATCCACA	69		
QY	1108	gaatgatctcttcttgcttcctcccaaaacaaagctttatcactatgttgtaataatgg	1167		
Db	70	GAATATATCTCTTGCTGTCATCCCAACCAAGAGCCTTTATTTACTCTGTGAACCAATGG	129		
QY	1168	gattcattgaagctattcccatgggggtccctatgtgtggagttcccatattgtgtatca	1227		
Db	130	GATCTATGAGCTATTTCACATGAGGATTCCTTATGTTGGGAATTCACATGTTGGTGATCA	189		
QY	1228	gcttgaatacatagctcacaatgaagagccaaagagcaagctgtlagaataaacttcaaac	1287		
Db	190	GCATGATATATATTTGCTGCTCTTAAGCTTAAGGGGCGACCTGTGAAATTAACCTGCCACAC	249		
QY	1288	tatgcaagcggaagatttactcgaagggtcttgaagaacatcattaccgattcccttataa	1347		
Db	250	AATGACGAGTCTGCTGCTTAATGCTTTGAGGAGCAACTTATTAACAACCCCTTCCTATAA	309		
QY	1348	agaagatgctatgaattatcaagaattcacatgatacactgtgaagcccttagatcg	1407		
Db	310	AGAAATATGCTATGAAGTTATCAAGAAATTCACCATGATCAACCTATTAAGCCCTTGACCG	369		
QY	1408	agcagctctcttgatcaggttctgtatcattcgccacaagaagagccaaagcactcgatcagc	1467		

QY	1059	aaacatcccatatgagagcaaatctgcgcgtctatgatgatacccaagaatgactctc	1118
Db	370	AGCAGCTTCTGGATTGATTTGTCTATGGGCCACCAAGAGCAACACACTGGGCCAGC	429
QY	1468	tgccatctgactccactcgtgtctccagcactactctatagatglatggttccctgtcagc	1527
Db	430	TTCCACGACGACTCCACTGGTACACAGTACACACTCTCTGATGTGATGGGTTCCGTCTGC	489
QY	1528	ctgtgtgagcaactgctatatctctgtgtccaaaatgttttttcttctgtcctaaat	1587
Db	490	TTGTGTGGCAACTATATATTTCTGGTCAATTAATTTCTGTGTTGTTGTTCAAGTT	549
QY	1588	taata 1592	
Db	550	TGCTA 554	
RESULT	13		
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DEFINITION	602588811n1 NIH_MGC_76	Homo sapiens	CDNA clone IMAGE:4722819 5',
ACCESSION	BG569536		mRNA sequence.
VERSION	BG569536.1	GI:13577189	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 728)		
JOURNAL	NIH-MGC http://mgs.ccl.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: CLONETECH Laboratories, Inc.		
	CDNA Library Preparation: CLONETECH Laboratories, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLCML581 row: f column: 04		
	High quality sequence stop: 699.		
FEATURES	Location/Qualifiers		
source	1..728		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:4722819"		
	/clone_11b="NIH_MGC_76"		
	/lab_host="DH10B (TI phage-resistant)"		
	/note="Organ: liver; Vector: pDNR-LIB (Clontech); site_1:		
	SfiI (ggcgccctcgcc); site_2: SfiI (ggcgatcatgccc); 5' and		
	3' adaptors used in cloning as follows: 5' adaptor		
	sequence: 5'-CACGCCCATTTTGGCC-3' and 3' adaptor		
	5'-ATTCTAGAGCCGAGCGAGCGCCGACATG-dT(30)TN-3' (where B = A,		
	C, or G and N = A, C, G, or T). Average insert size 1.8		
	kb (range 1.0-4.0 kb). 15/15 colonies contained inserts		
	by PCR. This library was enriched for full-length clones		
	and was constructed by Clontech Laboratories (Palo Alto,		
	CA). Note: this is a NIH-MGC Library."		
BASE COUNT	213 a 148 c 170 g 197 t		
ORIGIN			
Query Match	14.3%;	Score 395.4;	DB 155; Length 728;
Best Local Similarity	74.8%;	Pred. No. 5.5e-74;	
Matches 538; Conservative	0;	Mismatches 171;	Indels 10; Gaps 3.
QY	999	tatgtgcttcaagcccttgccagatcccaagaggtgtatcgtgagatcaaggaanaa	1058
Db	2	TAAATTGATACACCCCTGGCCCGAGATCCACAAAGGTTCTGTGGAGATTGTATGGGAATA	61

	BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (http://www.hsc.washington.edu) plate: 659 Row: J Column: 24 Seq primer: T7 Class: BAC ends High quality sequence stop: 552. Location/Qualifiers 1..552
FEATURES	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="Plate-659 Col-24 Row-J" /clone_lib="RPCI-11 Human Male BAC Library" /sex="male" /note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRV Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"
BASE COUNT	172 a 111 c 84 g 181 t 4 others
ORIGIN	
Query Match	14.3%; Score 394.8; DB 228; Length 552;
Best Local Similarity	91.8%; Pied No. 7.3e-74;
Matches 428; Conservative 0; Mismatches 37; Indels 1; Gaps 1	
OY 1806	gtgcttactcttcctcctaactttgtgcacaagaagcatgatataatctta 1865
Db 69	GGGCGCTTCTCTCTTTTGTCATTATTAACAAGGACGATTAACTACATTTCCGA 128
OY 1866	tctctgatatcaactgtcttcacatgaagtccattctctcaaccttaagtatggatgac 1925
Db 129	TTCCTGATNCAAGGTTCCTCATGATCTCATTCACTTTATTAACCTTAAGTGATGGGTGC 188
OY 1926	cftgcaatagctgattctcctggtgtgttgaccacaacacatgatgatgtlaaagaagtaaaatg 1985
Db 189	CYTCACTATGCGATTCCTCGGTGGTTCGCAAAACACATGATGATGAAGAATAAAAAATG 248
OY 1986	taaataccaacaatcagtaaacacacacacaaaatcaatgaagatctctgaatgaactt 2045
Db 249	TAAATTCACGAAATTCATCACTAACCACACAAATCAGTTAACATTCATG-CCTTAGCTT 307
OY 2046	gttatgagtaacataatgatcttctcttcttaaatlaaagaacctctacataccag 2105
Db 308	GTATGAGAAACATATATGATGTTTTTTTTCATTTAATAATAGCCCTCTCATATGCCAG 367
OY 2106	catlactgatlccagacaatgatattggtcaaabaabagataggatgggataactagaata 2165
Db 368	CATTAAGTATCTCACACACATGAAATTCCTTAATAATGACATAGAGCATACACTCAGAAAT 427
OY 2166	gtttcttatattccacataactcattatagatgltcatagtccttaactttctgcatactt 2225
Db 428	GTTTCTATATTTTCCACATACCTCATCTAGATGTCATGTGCATATTTCTGCCATCACTC 487
OY 2226	aactacatatttttgtgtgtcttgatataataagaagacttta 2271
Db 488	AACCAACATTTTGTTGTGTGCTCTGCATATATAAATAGACAGGCTCTCA 533
RESULT 15	
LOCUS	A1118428 761 bp mRNA EST 02-SEP-1998
DEFINITION	ue0e09.x1 Sugano mouse liver mla. Mus musculus cDNA clone IMAGE:1482856 3' similar to gb:x06558 mouse mRNA for UDP-glucuronosyltransferase (MOUSE);, mRNA sequence.
ACCESSION	A1118428
VERSION	A1118428.1 GI:3518752
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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